26. The method of claim 25, wherein said nucleic acid populations comprise nucleic acid populations from different subjects having a common trait of interest.

27. The method of claim 23, wherein said nucleic acid populations comprise one or more selected chromosomes.

28. The method of claim 23, wherein said nucleic acid populations comprise nucleic acid populations from different sources.

29. The method of claim 23, wherein said restriction fragments are size-selected prior to said amplifying step.

30. The method of claim 23, wherein part or all of said restriction fragments are cloned into a vector in a chromosome-specific and sequence-specific fashion.

31. The method of claim 23, wherein said adaptor sequence comprises a recognition site for mutHL.

32. The method of claim 31, wherein said adaptor sequence comprises a 5 base to 100 base long double-stranded DNA fragment.

33. The method of claim 32, wherein said DNA fragment comprises at least one GATC motif.

34. The method of claim 23, wherein said amplifying step further comprises using a polymerase chain reaction technique.

35. The method of claim 23, wherein said primer is complementary to at least a part of said adaptor sequence.

36. The method of claim 23, wherein said primer is labeled by a technique chosen from the group consisting of (a) adding a unique 5'-sequence to the primer; (b) adding a chemical activity to the primer which provides a means to distinguish between or among the amplification products from different said nucleic acid populations; and (c) adding modified nucleotides into the primer allowing one to distinguish between or among the amplification products from different said nucleic acid populations.

37. The method of claim 23, wherein identification of matched heterohybrids comprises the steps of:

(a) separating the homoduplexes from the heteroduplexes;

(b) identifying the mismatched heterohybrid fragments;

(c) eliminating the mismatched heterohybrid fragments; and

(d) identifying, isolating, or separating the fully-matched heterohybrid fragments.

38. The method of claim 37, wherein said eliminating step occurs via mismatch repair enzymes.

39. The method of claim 38, wherein said eliminating step comprises incubating the hybridization mixture with MutS, MutL, and MutH, resulting in a specific cleavage of mismatched hybrids.

40. The method of claim 38, wherein said eliminating step comprises:

(a) incubating the hybridization mixture with MutS; and

(b) contacting the resulting product with a MutS-binding material.

41. The method of claim 37, wherein said separating step comprises separating heterohybrids from homohybrids based upon labeling of primers.

42. The method of claim 41, wherein the separating step based upon labeling of primers comprises the steps of:

(a) separately amplifying restriction fragments using a primer with a unique 5' sequence for each of one or more nucleic acid populations;

(b) mixing the amplification products from said nucleic acid populations carrying unique 5' ends;

(c) denaturing said amplification products;

(d) rehybridizing said amplification products;

(e) digesting perfectly-matched (blunt-ended) deoxyribonucleic acids by ExoIII; and

(f) eliminating the ExoIII-created single strands.

43. The method of claim 42, wherein said eliminating step comprises binding said ExoIII-created single strands to a single strand specific matrix.

44. The method of claim 37, wherein said separating step comprises separating the heterohybrids from homohybrids based upon methylation of one of two nucleic acid preparations.

45. The method of claim 37, wherein said separating step comprises separating the heterohybrids from homohybrids based upon methylation of one of two groups of restriction fragments.

46. A kit suitable for genetic analysis according to the method of claim 23, comprising:

(a) a double stranded adaptor molecule; and

(b) a specific, labeled primer.

47. The kit of claim 46, further comprising control deoxyribonucleic acids.

48. The kit of claim 46, further comprising control enzymes.

49. The kit of claim 46, further comprising a means for the detection of selected DNA fragments.

50. The kit of claim 49, wherein said means comprises an ordered DNA array.

51. The kit of claim 49, wherein said means comprises coded beads carrying specific DNA sequences.

52. A method of separating identical DNA fragments from complex mixtures of at least two nucleic acid populations, comprising:

(a) hybridizing the populations; and

(b) separating the fully-matched heterohybrids formed via the hybridization;

wherein said nucleic acid populations comprise amplified nucleic acids.

53. A method of identifying DNA regions that are relevant to a pathological condition or a particular trait, comprising:

(a) hybridizing at least two nucleic acid populations from different sources having the particular trait or pathology; and

(b) separating the fully-matched heterohybrids formed which contain DNA regions that are relevant to said pathological condition or particular trait;

wherein said nucleic acid populations are chosen from the group consisting of amplified nucleic acids and pre-selected nucleic acids.